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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: John Craig Smith

Serial No.: 09/773,599

Filed: February 2, 2001

Title

: DIAGNOSTIC METHOD

Commissioner for Patents Washington, D.C. 20231

Art Unit: 1634

Examiner: Juliet C. Einsmann

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RESPONSE TO RESTRICTION REQUIREMENT

Responsive to the action mailed May 13, 2002, applicant elects the invention of Group I and further elects the single nucleotide polymorphism at position 33251 of the reverse complement of EMBL Accession Number AC006953. This polymorphism is represented by SEQ ID NO:4. This election is made with traverse.

First, Applicants point out that all of the polymorphisms specified in the claims relate to a single gene and its encoded protein, uPAR. It is not clear from the language of the restriction requirement that the Examiner appreciated this fact. For example, see page 3, line 8, where the Examiner stated that the various polymorphic sequences are "unrelated". When the gene is viewed as a whole, the various polymorphisms are of course highly related. Furthermore, from a practical standpoint, a single search will reveal the art relevant to all of these polymorphisms, including the methods of detecting them. Thus, there would certainly not be an undue burden on the examiner to search all eight nucleotide polymorphisms and two amino acid residue polymorphisms, as well as all methods of detecting them.

Second, the restriction between a given nucleotide polymorphism and its corresponding amino acid residue polymorphism seems particularly unwarranted. The polymorphism at nucleotide position 33251 of the reverse complement of EMBL Accession Number AC006953 corresponds to the polymorphism at amino acid residue 198 of the uPAR protein; i.e., anyone

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with a polymorphism at residue 198 will also have a polymorphism at nucleotide position 332521. Thus, a search that encompasses one will be adequate to cover the other. The same is true of nucleotide position 36623 and amino acid residue 295. Again, there is no burden on the examiner to search the polymorphism at both the nucleic acid and the amino acid levels. It would seem odd to separate them.

Third, Applicant notes that both groups I and II are classified in class 435, while groups IV, V, and VI are all in class 424. It would appear that groups I and II can be efficiently searched together, and likewise groups IV, V, and VI.

Finally, applicant points out that claim 1 covers determining the sequence "at one or more" of the eight nucleotide positions and two amino acid residue positions. If the restriction requirement is allowed to stand, it will limit applicant to claiming a method of determining the sequence at only a <u>single one</u> of the ten positions. The restriction requirement ignores those embodiments of the claims in which the sequence at two, three, four, five, six, seven, eight, nine or all ten positions is determined. It essentially prohibits applicants from presenting such claims, in this application or any divisional.

Applicants strongly protest and request withdrawal of the restriction requirement.

Enclosed is an Associate Power of Attorney granting Power of Attorney to the undersigned and requesting that future communications be direct to the undersigned. Also enclosed is a Petition for Extension of Time for one month and a check for the required fee of \$110. Please apply any other charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date.

Janis K. Fraser, Ph.D., J.D.

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